Claim Amendments

Claim 1 (withdrawn): A method for analyzing a nucleic acid sample comprised of the steps:

(a) forming labeled DNA sample fragments from a nucleic acid sample;

(b) size separating said sample fragments with size standard fragments, and detecting the fragments to form a sample signal and a size standard signal;

(c) transforming the sample signal into size coordinates using the size standard signal; and

(d) analyzing the nucleic acid sample in size coordinates.

Claim 2 (withdrawn): A method for analyzing a nucleic acid sample comprised of the steps:

(a) forming labeled DNA sample fragments from a nucleic acid sample;

(b) size separating and detecting said sample fragments to form a sample signal;

(c) forming labeled DNA ladder fragments corresponding to molecular lengths;

(d) size separating and detecting said ladder fragments to form a ladder signal;

(e) transforming the sample signal into length coordinates using the ladder signal; and

(f) analyzing the nucleic acid sample signal in length coordinates.

Claim 3 (withdrawn): A method as described in Claim 2 wherein after the analyzing step (f) there is the additional step of determining a length or amount of a fragment in the nucleic acid sample.

Claim 4 (withdrawn): A method as described in Claim 3 wherein after the determining step there is the additional step of finding a gene by positional cloning.

Claim 5 (withdrawn): A method as described in Claim 3 wherein after the determining step there is the additional step of identifying an individual by DNA profiling.

Claim 6 (withdrawn): A method for generating revenue from computer scoring of genetic data comprised of the steps:

(a) supplying a software program that automatically scores genetic data;

(b) forming genetic data that can be scored by the software program;

(c) scoring the genetic data using the software program to form a quantity of genetic data; and

(d) generating a revenue from computer scoring of genetic data that is related to the quantity.

Claim 7 (withdrawn): A method as described in Claim 6 wherein prior to the step (d) of generating a revenue there are the steps of:

(e) defining a labor cost of scoring the quantity of genetic data when not using the software program;

(f) providing a calculating mechanism for estimating the labor cost from the quantity;

(g) determining the labor cost based on the quantity; and

(h) establishing a price for using the software program that is related to the labor cost.

Claim 8 (withdrawn): A method as described in Claim 7 wherein the calculating mechanism includes a spreadsheet.

Claim 9 (withdrawn): A method as described in Claim 7 wherein the calculating mechanism is provided via the Internet.

Claim 10 (withdrawn): A method as described in Claim 7 wherein the calculating mechanism operates interactively via the Internet.

Claim 11 (withdrawn): A system for analyzing a nucleic acid sample comprising:

(a) means for forming labeled DNA sample fragments from a nucleic acid sample;

(b) means for size separating and detecting said sample fragments to form a sample signal, said separating and detecting means in communication with the sample fragments;

(c) means for forming labeled DNA ladder fragments corresponding to molecular lengths;

(d) means for size separating and detecting said ladder fragments to form a ladder signal, said separating and detecting means in communication with the ladder fragments;

Serial Number: 09/504,389

(e) means for transforming the sample signal into length coordinates using the ladder signal, said transforming means in communication with the signals; and

(f) means for analyzing the nucleic acid sample signal in length coordinates, said analyzing means in communication with the transforming means.

Claim 12 (withdrawn): A method for producing a nucleic acid analysis comprised of the steps:

(a) analyzing a first nucleic acid sample on a first size separation instrument to form a first signal;

(b) analyzing a second nucleic acid sample on a second size separation instrument to form a second signal;

(c) comparing the first signal with the second signal in a computing device with memory to form a comparison; and

(d) producing a nucleic acid analysis of the two samples from the comparison that is independent of the size separation instruments used.

Claim 13 (withdrawn): A method as described in Claim 12 wherein the size separation instrument is a DNA sequencer that uses electrophoresis.

Claim 14 (withdrawn): A method as described in Claim 12 wherein the nucleic acid analysis characterizes a size or amount of DNA in one of the nucleic acid samples.

Claim 15 (withdrawn): A method as described in Claim 12 wherein the nucleic acid analysis finds a gene by positional cloning.

Claim 16 (withdrawn): A method as described in Claim 12 wherein the nucleic acid analysis identifies an individual by DNA profiling.

Claim 17 (previously presented): A method for analyzing a DNA mixture comprised of the steps:

(a) obtaining DNA profile data of a sample that comprises a DNA mixture of two or more individuals;

(b) representing the data and a genotype of the individuals contained in the DNA mixture in a set of linear equations;

(c) deriving a mathematical solution by performing a matrix operation on the linear equations; and

(d) determining the genotype at a locus of an individual contained in the DNA mixture from the mathematical solution.

Claim 18 (previously presented): A method as described in Claim 17 wherein the obtaining step (a) includes the step of performing a PCR on an STR locus of an individual.

Claim 19 (previously presented): A method as described in Claim 17 wherein the representing step (b) includes a matrix or vector representation of the set of linear equations.

Claim 20 (previously presented): A method as described in Claim 17 wherein the deriving step (c) includes an optimization procedure.

Claim 21 (canceled): A method as described in Claim 17 wherein the deriving step (c) includes performing a matrix operation on the linear equations.

Claim 22 (previously presented): A method as described in Claim 17 wherein the determining step (d) produces an estimate of the genotype of an individual.

Claim 23 (previously presented): A method as described in Claim 17 wherein the determining step (d) produces an estimate of a proportion or weight of an individual's DNA contained in the DNA mixture.

Claim 24 (previously presented): A method as described in Claim 17 wherein the determining step (d) produces an estimate of the quality of the determined solution.

Claim 25 (previously presented): A method as described in Claim 19 wherein the matrix representation has a term that includes a matrix multiplication of a genotype matrix and a weight matrix.

Claim 26 (previously presented): A method as described in Claim 22 wherein after the determining step (d), the estimated genotype is matched against a suspect genotype.

Claim 27 (previously presented): A method as described in Claim 26 wherein the suspect genotype is drawn from a database of candidate suspect genotypes.

Claim 28 (previously presented): A method as described in Claim 26 wherein the suspect is a likely perpetrator of a crime.

Claim 29 (previously presented): A method as described in Claim 20 wherein the optimization procedure includes a minimization step.

Claim 30 (previously presented): A method as described in Claim 20 wherein the optimization procedure includes an arithmetic operation.

Claim 31 (new): A method as described in Claim 17 wherein the determining step (d) jointly produces both an estimate of a proportion or weight of an individual's DNA contained in the DNA mixture and an estimate of the genotype of the individual.